

1
SEQUENCE LISTING

<110> Babiychuk, Elena
Kushnir, Sergei
De Block, Marc
Inze, Dirk

<120> Methods and means to modulate programmed cell death in eukaryotic cells

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<170> PatentIn Ver. 2.0

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 Thr Glu Arg Phe Gln Lys Phe Ala Ser Thr Arg Asn Arg Met Leu Leu
 485 490 495

tgg cat ggt tct cgg ttg agc aac tgg gct ggg atc ctt tct cag ggt 1651
 Trp His Gly Ser Arg Leu Ser Asn Trp Ala Gly Ile Leu Ser Gln Gly
 500 505 510 515

ctg cga atc gct cct cct gaa gca cct gtt act ggt tac atg ttt ggc 1699
 Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly
 520 525 530

aag ggt gtt tac ttt gct gac atg ttt tca aag agt gca aac tat tgc 1747
 Lys Gly Val Tyr Phe Ala Asp Met Phe Ser Lys Ser Ala Asn Tyr Cys
 535 540 545

tac gcc tct gaa gca tgt aga tct gga gta ctg ctt tta tgt gag gtt 1795
 Tyr Ala Ser Glu Ala Cys Arg Ser Gly Val Leu Leu Cys Glu Val
 550 555 560

gca ttg ggc gat atg aat gag cta ctg aat gca gat tac gat gct aat 1843
 Ala Leu Gly Asp Met Asn Glu Leu Leu Asn Ala Asp Tyr Asp Ala Asn
 565 570 575

aac ctg ccc aaa gga aaa tta aga tcc aag gga gtt ggt caa aca gca 1891
 Asn Leu Pro Lys Gly Lys Leu Arg Ser Lys Gly Val Gly Gln Thr Ala
 580 585 590 595

cct aac atg gtc gag tct aag gtc gct gac gat ggt gtt gtt gtt ccc 1939
 Pro Asn Met Val Glu Ser Lys Val Ala Asp Asp Gly Val Val Val Pro
 600 605 610

ctt ggc gaa ccc aaa cag gaa cct tcc aaa agg ggt ggc ttg ctt tat 1987
 Leu Gly Glu Pro Lys Gln Glu Pro Ser Lys Arg Gly Gly Leu Leu Tyr
 615 620 625

aat gag tac ata gtg tac aac gta gac cag ata aga atg cgg tat gtc 2035
 Asn Glu Tyr Ile Val Tyr Asn Val Asp Gln Ile Arg Met Arg Tyr Val
 630 635 640

tta cat gtt aac ttc aat ttc aag aga cgg tag atgttgcaaa gagctgaaac 2088
 Leu His Val Asn Phe Asn Phe Lys Arg Arg
 645 650

tggtgctgag atcttagcag aacatatgtg gacttatagc accaggtgcc ctcagcctca 2148

ttttctgagc aaatttggtg gcctttgcat ttcgattttg gtttcagctt ctagcccat 2208

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<211> 653

<212> PRT

<213> Zea mays

<400> 4

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 Asp Ala Ala Ile Cys Glu Ala Glu Lys Ala Val Val Ala Ala Ala Pro
 35 40 45
 Thr Ser Val Ala Asn Gly Tyr Asp Val Ala Val Asp Gly Lys Arg Asn
 50 55 60
 Cys Gly Asn Asn Lys Arg Lys Arg Ser Gly Asp Gly Gly Glu Glu Gly
 65 70 75 80
 Asn Gly Asp Thr Cys Thr Asp Val Thr Lys Leu Glu Gly Met Ser Tyr
 85 90 95
 Arg Glu Leu Gln Gly Leu Ala Lys Ala Arg Gly Val Ala Ala Asn Gly
 100 105 110
 Gly Lys Lys Asp Val Ile Gln Arg Leu Leu Ser Ala Thr Ala Gly Pro
 115 120 125
 Ala Ala Val Ala Asp Gly Gly Pro Leu Gly Ala Lys Glu Val Ile Lys
 130 135 140
 Gly Gly Asp Glu Glu Val Glu Val Lys Lys Glu Lys Met Val Thr Ala
 145 150 155 160
 Thr Lys Lys Gly Ala Ala Val Leu Asp Gln His Ile Pro Asp His Ile
 165 170 175
 Lys Val Asn Tyr His Val Leu Gln Val Gly Asp Glu Ile Tyr Asp Ala
 180 185 190
 Thr Leu Asn Gln Thr Asn Val Gly Asp Asn Asn Asn Lys Phe Tyr Ile
 195 200 205
 Ile Gln Val Leu Glu Ser Asp Ala Gly Gly Ser Phe Met Val Tyr Asn
 210 215 220
 Arg Trp Gly Arg Val Gly Val Arg Gly Gln Asp Lys Leu His Gly Pro
 225 230 235 240
 Ser Pro Thr Arg Asp Gln Ala Ile Tyr Glu Phe Glu Gly Lys Phe His
 245 250 255
 Asn Lys Thr Asn Asn His Trp Ser Asp Arg Lys Asn Phe Lys Cys Tyr
 260 265 270
 Ala Lys Lys Tyr Thr Trp Leu Glu Met Asp Tyr Gly Glu Thr Glu Lys
 275 280 285
 Glu Ile Glu Lys Gly Ser Ile Thr Asp Gln Ile Lys Glu Thr Lys Leu
 290 295 300
 Glu Thr Arg Ile Ala Gln Phe Ile Ser Leu Ile Cys Asn Ile Ser Met
 305 310 315 320
 Met Lys Gln Arg Met Val Glu Ile Gly Tyr Asn Ala Glu Lys Leu Pro
 325 330 335
 Leu Gly Lys Leu Arg Lys Ala Thr Ile Leu Lys Gly Tyr His Val Leu
 340 345 350

Lys Arg Ile Ser Asp Val Ile Ser Lys Ala Asp Arg Arg His Leu Glu
 355 360 365
 Gln Leu Thr Gly Glu Phe Tyr Thr Val Ile Pro His Asp Phe Gly Phe
 370 375 380
 Arg Lys Met Arg Glu Phe Ile Ile Asp Thr Pro Gln Lys Leu Lys Ala
 385 390 395 400
 Lys Leu Glu Met Val Glu Ala Leu Gly Glu Ile Glu Ile Ala Thr Lys
 405 410 415
 Leu Leu Glu Asp Asp Ser Ser Asp Gln Asp Asp Pro Leu Tyr Ala Arg
 420 425 430
 Tyr Lys Gln Leu His Cys Asp Phe Thr Pro Leu Glu Ala Asp Ser Asp
 435 440 445
 Glu Tyr Ser Met Ile Lys Ser Tyr Leu Arg Asn Thr His Gly Lys Thr
 450 455 460
 His Ser Gly Tyr Thr Val Asp Ile Val Gln Ile Phe Lys Val Ser Arg
 465 470 475 480
 His Gly Glu Thr Glu Arg Phe Gln Lys Phe Ala Ser Thr Arg Asn Arg
 485 490 495
 Met Leu Leu Trp His Gly Ser Arg Leu Ser Asn Trp Ala Gly Ile Leu
 500 505 510
 Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr
 515 520 525
 Met Phe Gly Lys Gly Val Tyr Phe Ala Asp Met Phe Ser Lys Ser Ala
 530 535 540
 Asn Tyr Cys Tyr Ala Ser Glu Ala Cys Arg Ser Gly Val Leu Leu Leu
 545 550 555 560
 Cys Glu Val Ala Leu Gly Asp Met Asn Glu Leu Leu Asn Ala Asp Tyr
 565 570 575
 Asp Ala Asn Asn Leu Pro Lys Gly Lys Leu Arg Ser Lys Gly Val Gly
 580 585 590
 Gln Thr Ala Pro Asn Met Val Glu Ser Lys Val Ala Asp Asp Gly Val
 595 600 605
 Val Val Pro Leu Gly Glu Pro Lys Gln Glu Pro Ser Lys Arg Gly Gly
 610 615 620
 Leu Leu Tyr Asn Glu Tyr Ile Val Tyr Asn Val Asp Gln Ile Arg Met
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<211> 2147

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (129)..(2042)

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 agacgaaa atg gcg aac aag ctc aaa gtc gac gaa ctc cgt tta aaa ctc 170
 Met Ala Asn Lys Leu Lys Val Asp Glu Leu Arg Leu Lys Leu
 1 5 10
 gcc gag cgt gga ctc agt act act gga gtc aaa gcc gtt ctg gtg gag 218
 Ala Glu Arg Gly Leu Ser Thr Thr Gly Val Lys Ala Val Leu Val Glu
 15 20 25 30
 agg ctt gaa gag gct atc gca gaa gac act aag aag gaa gaa tca aag 266
 Arg Leu Glu Glu Ala Ile Ala Glu Asp Thr Lys Lys Glu Glu Ser Lys
 35 40 45
 agc aag agg aaa aga aat tct tct aat gat act tat gaa tcg aac aaa 314
 Ser Lys Arg Lys Arg Asn Ser Ser Asn Asp Thr Tyr Glu Ser Asn Lys
 50 55 60
 ttg att gca att ggc gaa ttt cgt ggg atg att gtg aag gaa ttg cgt 362
 Leu Ile Ala Ile Gly Glu Phe Arg Gly Met Ile Val Lys Glu Leu Arg
 65 70 75
 gag gaa gct att aag aga ggc tta gat aca aca gga acc aaa aag gat 410
 Glu Glu Ala Ile Lys Arg Gly Leu Asp Thr Thr Gly Thr Lys Lys Asp
 80 85 90
 ctt ctt gag agg ctt tgc aat gat gct aat aac gtt tcc aat gca cca 458
 Leu Leu Glu Arg Leu Cys Asn Asp Ala Asn Asn Val Ser Asn Ala Pro
 95 100 105 110
 gtc aaa tcc agt aat ggg aca gat gaa gct gaa gat gac aac aat ggc 506
 Val Lys Ser Ser Asn Gly Thr Asp Glu Ala Glu Asp Asp Asn Asn Gly
 115 120 125
 ttt gaa gaa gaa aag aaa gaa gag aaa atc gta acc gcg aca aag aag 554
 Phe Glu Glu Glu Lys Lys Glu Glu Lys Ile Val Thr Ala Thr Lys Lys
 130 135 140
 ggt gca gcg gtg cta gat cag tgg att cct gat gag ata aag agt cag 602
 Gly Ala Ala Val Leu Asp Gln Trp Ile Pro Asp Glu Ile Lys Ser Gln
 145 150 155
 tac cat gtt cta caa agg ggt gat gat gtt tat gat gct atc tta aat 650
 Tyr His Val Leu Gln Arg Gly Asp Asp Val Tyr Asp Ala Ile Leu Asn
 160 165 170
 cag aca aat gtc agg gat aat aat aac aag ttc ttt gtc cta caa gtc 698
 Gln Thr Asn Val Arg Asp Asn Asn Asn Lys Phe Phe Val Leu Gln Val
 175 180 185 190
 cta gag tcg gat agt aaa aag aca tac atg gtt tac act aga tgg gga 746
 Leu Glu Ser Asp Ser Lys Lys Thr Tyr Met Val Tyr Thr Arg Trp Gly
 195 200 205
 aga gtt ggt gtg aaa gga caa agt aag cta gat ggg cct tat gac tca 794
 Arg Val Gly Val Lys Gly Gln Ser Lys Leu Asp Gly Pro Tyr Asp Ser
 210 215 220
 tgg gat cgt gcg ata gag ata ttt acc aat aag ttc aat gac aag aca 842
 Trp Asp Arg Ala Ile Glu Ile Phe Thr Asn Lys Phe Asn Asp Lys Thr
 225 230 235
 aag aat tat tgg tct gac aga aag gag ttt atc cca cat ccc aag tcc 890
 Lys Asn Tyr Trp Ser Asp Arg Lys Glu Phe Ile Pro His Pro Lys Ser

240	245	250	
tat aca tgg ctc gaa atg gat tac gga aaa gag gaa aat gat tca ccg Tyr Thr Trp Leu Glu Met Asp Tyr Gly Lys Glu Glu Asn Asp Ser Pro 255 260 265 270			938
gtc aat aat gat att ccg agt tca tct tcc gaa gtt aaa cct gaa caa Val Asn Asn Asp Ile Pro Ser Ser Ser Ser Glu Val Lys Pro Glu Gln 275 280 285			986
tca aaa cta gat act cgg gtt gcc aag ttc atc tct ctt ata tgt aat Ser Lys Leu Asp Thr Arg Val Ala Lys Phe Ile Ser Leu Ile Cys Asn 290 295 300			1034
gtc agc atg atg gca cag cat atg atg gaa ata gga tat aac gct aac Val Ser Met Met Ala Gln His Met Met Glu Ile Gly Tyr Asn Ala Asn 305 310 315			1082
aaa ttg cca ctc ggc aag ata agc aag tcc aca att tca aag ggt tat Lys Leu Pro Leu Gly Lys Ile Ser Lys Ser Thr Ile Ser Lys Gly Tyr 320 325 330			1130
gaa gtg ctg aag aga ata tcg gag gtg att gac cgg tat gat aga acg Glu Val Leu Lys Arg Ile Ser Glu Val Ile Asp Arg Tyr Asp Arg Thr 335 340 345 350			1178
agg ctt gag gaa ctg agt gga gag ttc tac aca gtg ata cct cat gat Arg Leu Glu Glu Leu Ser Gly Glu Phe Tyr Thr Val Ile Pro His Asp 355 360 365			1226
ttt ggt ttt aag aaa atg agt cag ttt gtt ata gac act cct caa aag Phe Gly Phe Lys Lys Met Ser Gln Phe Val Ile Asp Thr Pro Gln Lys 370 375 380			1274
ttg aaa cag aaa att gaa atg gtt gaa gca tta ggt gaa att gaa ctc Leu Lys Gln Lys Ile Glu Met Val Glu Ala Leu Gly Glu Ile Glu Leu 385 390 395			1322
gca aca aag ttg ttg tcc gtc gac ccg gga ttg cag gat gat cct tta Ala Thr Lys Leu Leu Ser Val Asp Pro Gly Leu Gln Asp Asp Pro Leu 400 405 410			1370
tat tat cac tac cag caa ctt aat tgt ggt ttg acg cca gta gga aat Tyr Tyr His Tyr Gln Gln Leu Asn Cys Gly Leu Thr Pro Val Gly Asn 415 420 425 430			1418
gat tca gag gag ttc tct atg gtt gct aat tac atg gag aac act cat Asp Ser Glu Glu Phe Ser Met Val Ala Asn Tyr Met Glu Asn Thr His 435 440 445			1466
gca aag acg cat tcg gga tat acg gtt gag att gcc caa cta ttt aga Ala Lys Thr His Ser Gly Tyr Thr Val Glu Ile Ala Gln Leu Phe Arg 450 455 460			1514
gct tcg aga gct gtt gaa gct gat cga ttc caa cag ttt tca agt tcg Ala Ser Arg Ala Val Glu Ala Asp Arg Phe Gln Gln Phe Ser Ser Ser 465 470 475			1562
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act ggt tac atg ttt gga aaa ggg gtt tac ttt gcg gat atg ttc tcc			1706

Thr Gly Tyr Met Phe Gly Lys Gly Val Tyr Phe Ala Asp Met Phe Ser
515 520 525

aag agt gcg aac tat tgc tat gcc aac act ggc gct aat gat ggc gtt 1754
Lys Ser Ala Asn Tyr Cys Tyr Ala Asn Thr Gly Ala Asn Asp Gly Val
530 535 540

ctg ctc ctc tgc gag gtt gct ttg gga gac atg aat gaa ctt ctg tat 1802
Leu Leu Leu Cys Glu Val Ala Leu Gly Asp Met Asn Glu Leu Leu Tyr
545 550 555

tca gat tat aac gcg gat aat cta ccc ccg gga aag cta agc aca aaa 1850
Ser Asp Tyr Asn Ala Asp Asn Leu Pro Pro Gly Lys Leu Ser Thr Lys
560 565 570

ggt gtg ggg aaa aca gca cca aac cca tca gag gct caa aca cta gaa 1898
Gly Val Gly Lys Thr Ala Pro Asn Pro Ser Glu Ala Gln Thr Leu Glu
575 580 585 590

gac ggt gtt gtt gtt cca ctt ggc aaa cca gtg gaa cgt tca tgc tcc 1946
Asp Gly Val Val Val Pro Leu Gly Lys Pro Val Glu Arg Ser Cys Ser
595 600 605

aag ggg atg ttg ttg tac aac gaa tat ata gtc tac aat gtg gaa caa 1994
Lys Gly Met Leu Leu Tyr Asn Glu Tyr Ile Val Tyr Asn Val Glu Gln
610 615 620

atc aag atg cgt tat gtg atc caa gtc aaa ttc aac tac aag cac taa 2042
Ile Lys Met Arg Tyr Val Ile Gln Val Lys Phe Asn Tyr Lys His
625 630 635

aacttatgta tattagcttt tgaacatcaa ctaattatcc aaaaatcagc gttttattgt 2102

atttcttttca aactccttca tctctgattt tgcacggttc actcg 2147

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<211> 637

<212> PRT

<213> Arabidopsis thaliana

<400> 6

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Glu Glu Ala Ile Ala Glu Asp Thr Lys Lys Glu Glu Ser Lys Ser Lys
35 40 45

Arg Lys Arg Asn Ser Ser Asn Asp Thr Tyr Glu Ser Asn Lys Leu Ile
50 55 60

Ala Ile Gly Glu Phe Arg Gly Met Ile Val Lys Glu Leu Arg Glu Glu
65 70 75 80

Ala Ile Lys Arg Gly Leu Asp Thr Thr Gly Thr Lys Lys Asp Leu Leu
85 90 95

Glu Arg Leu Cys Asn Asp Ala Asn Asn Val Ser Asn Ala Pro Val Lys
100 105 110

Ser Ser Asn Gly Thr Asp Glu Ala Glu Asp Asp Asn Asn Gly Phe Glu
115 120 125

Glu Glu Lys Lys Glu Glu Lys Ile Val Thr Ala Thr Lys Lys Gly Ala

Ala	Val	Leu	Asp	Gln	Trp	Ile	Pro	Asp	Glu	Ile	Lys	Ser	Gln	Tyr	His
145					150				155						160
Val	Leu	Gln	Arg	Gly	Asp	Asp	Val	Tyr	Asp	Ala	Ile	Leu	Asn	Gln	Thr
				165					170					175	
Asn	Val	Arg	Asp	Asn	Asn	Asn	Lys	Phe	Phe	Val	Leu	Gln	Val	Leu	Glu
			180					185					190		
Ser	Asp	Ser	Lys	Lys	Thr	Tyr	Met	Val	Tyr	Thr	Arg	Trp	Gly	Arg	Val
		195					200					205			
Gly	Val	Lys	Gly	Gln	Ser	Lys	Leu	Asp	Gly	Pro	Tyr	Asp	Ser	Trp	Asp
	210					215					220				
Arg	Ala	Ile	Glu	Ile	Phe	Thr	Asn	Lys	Phe	Asn	Asp	Lys	Thr	Lys	Asn
225					230					235					240
Tyr	Trp	Ser	Asp	Arg	Lys	Glu	Phe	Ile	Pro	His	Pro	Lys	Ser	Tyr	Thr
				245					250					255	
Trp	Leu	Glu	Met	Asp	Tyr	Gly	Lys	Glu	Glu	Asn	Asp	Ser	Pro	Val	Asn
			260					265					270		
Asn	Asp	Ile	Pro	Ser	Ser	Ser	Ser	Glu	Val	Lys	Pro	Glu	Gln	Ser	Lys
		275					280					285			
Leu	Asp	Thr	Arg	Val	Ala	Lys	Phe	Ile	Ser	Leu	Ile	Cys	Asn	Val	Ser
	290					295					300				
Met	Met	Ala	Gln	His	Met	Met	Glu	Ile	Gly	Tyr	Asn	Ala	Asn	Lys	Leu
305					310					315					320
Pro	Leu	Gly	Lys	Ile	Ser	Lys	Ser	Thr	Ile	Ser	Lys	Gly	Tyr	Glu	Val
				325					330					335	
Leu	Lys	Arg	Ile	Ser	Glu	Val	Ile	Asp	Arg	Tyr	Asp	Arg	Thr	Arg	Leu
			340					345					350		
Glu	Glu	Leu	Ser	Gly	Glu	Phe	Tyr	Thr	Val	Ile	Pro	His	Asp	Phe	Gly
		355					360					365			
Phe	Lys	Lys	Met	Ser	Gln	Phe	Val	Ile	Asp	Thr	Pro	Gln	Lys	Leu	Lys
	370					375					380				
Gln	Lys	Ile	Glu	Met	Val	Glu	Ala	Leu	Gly	Glu	Ile	Glu	Leu	Ala	Thr
385					390					395					400
Lys	Leu	Leu	Ser	Val	Asp	Pro	Gly	Leu	Gln	Asp	Asp	Pro	Leu	Tyr	Tyr
				405					410					415	
His	Tyr	Gln	Gln	Leu	Asn	Cys	Gly	Leu	Thr	Pro	Val	Gly	Asn	Asp	Ser
			420					425					430		
Glu	Glu	Phe	Ser	Met	Val	Ala	Asn	Tyr	Met	Glu	Asn	Thr	His	Ala	Lys
		435					440					445			
Thr	His	Ser	Gly	Tyr	Thr	Val	Glu	Ile	Ala	Gln	Leu	Phe	Arg	Ala	Ser
	450					455					460				
Arg	Ala	Val	Glu	Ala	Asp	Arg	Phe	Gln	Gln	Phe	Ser	Ser	Ser	Lys	Asn
465					470					475					480
Arg	Met	Leu	Leu	Trp	His	Gly	Ser	Arg	Leu	Thr	Asn	Trp	Ala	Gly	Ile
				485					490					495	

Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly
500 505 510

Tyr Met Phe Gly Lys Gly Val Tyr Phe Ala Asp Met Phe Ser Lys Ser
515 520 525

Ala Asn Tyr Cys Tyr Ala Asn Thr Gly Ala Asn Asp Gly Val Leu Leu
530 535 540

Leu Cys Glu Val Ala Leu Gly Asp Met Asn Glu Leu Leu Tyr Ser Asp
545 550 555 560

Tyr Asn Ala Asp Asn Leu Pro Pro Gly Lys Leu Ser Thr Lys Gly Val
565 570 575

Gly Lys Thr Ala Pro Asn Pro Ser Glu Ala Gln Thr Leu Glu Asp Gly
580 585 590

Val Val Val Pro Leu Gly Lys Pro Val Glu Arg Ser Cys Ser Lys Gly
595 600 605

Met Leu Leu Tyr Asn Glu Tyr Ile Val Tyr Asn Val Glu Gln Ile Lys
610 615 620

Met Arg Tyr Val Ile Gln Val Lys Phe Asn Tyr Lys His
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<210> 7

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: A domain of non-conventional PARP proteins

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Arg Gly Xaa Xaa Xaa Xaa Gly Xaa Lys Xaa Xaa Xaa Xaa Arg Leu
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<210> 8

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: A1 domain on non conventional PARP protein

<400> 8

Xaa Leu Xaa Val Xaa Xaa Xaa Arg Xaa Xaa Leu Xaa Xaa Arg Gly Leu
1 5 10 15

Xaa Xaa Xaa Gly Val Lys Xaa Xaa Leu Val Xaa Arg Leu Xaa Xaa Ala
20 25 30

Ile

<210> 9

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: A2 domain of non-conventional PARP protein

<400> 9

Gly Met Xaa Xaa Xaa Glu Leu Xaa Xaa Xaa Ala Xaa Xaa Arg Gly Xaa
 1 5 10 15

Xaa Xaa Xaa Gly Xaa Lys Lys Asp Xaa Xaa Arg Leu Xaa Xaa
 20 25 30

<210> 10

<211> 3212

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (81)..(3020)

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aaccacagca ggccggcgca atg gcg gcg ccg cca aag gcg tgg aag gcg gag 113
 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu
 1 5 10

tat gcc aag tct ggg cgg gcc tcg tgc aag tca tgc cgg tcc cct atc 161
 Tyr Ala Lys Ser Gly Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile
 15 20 25

gcc aag gac cag ctc cgt ctt ggc aag atg gtt cag gcg tca cag ttc 209
 Ala Lys Asp Gln Leu Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe
 30 35 40

gac ggc ttc atg ccg atg tgg aac cat gcc agg tgc atc ttc agc aag 257
 Asp Gly Phe Met Pro Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys
 45 50 55

aag aac cag ata aaa tcc gtt gac gat gtt gaa ggg ata gat gca ctt 305
 Lys Asn Gln Ile Lys Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu
 60 65 70 75

aga tgg gat gat caa gag aag ata cga aac tac gtt ggg agt gcc tca 353
 Arg Trp Asp Asp Gln Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser
 80 85 90

gct ggt aca agt tct aca gct gct cct cct gag aaa tgt aca att gag 401
 Ala Gly Thr Ser Ser Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu
 95 100 105

att gct cca tct gcc cgt act tca tgt aga cga tgc agt gaa aag att 449
 Ile Ala Pro Ser Ala Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile
 110 115 120

aca aaa gga tcg gtc cgt ctt tca gct aag ctt gag agt gaa ggt ccc 497
 Thr Lys Gly Ser Val Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro
 125 130 135

aag ggt ata cca tgg tat cat gcc aac tgt ttc ttt gag gta tcc ccg 545
 Lys Gly Ile Pro Trp Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro
 140 145 150 155

tct gca act gtt gag aag ttc tca ggc tgg gat act ttg tcc gat gag 593
 Ser Ala Thr Val Glu Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu

160

165 170

gat aag aga acc atg ctc gat ctt gtt aaa aaa gat gtt ggc aac aat	641
Asp Lys Arg Thr Met Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn	
175 180 185	
gaa caa aat aag ggt tcc aag cgc aag aaa agt gaa aat gat att gat	689
Glu Gln Asn Lys Gly Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp	
190 195 200	
agc tac aaa tcc gcc agg tta gat gaa agt aca tct gaa ggt aca gtg	737
Ser Tyr Lys Ser Ala Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val	
205 210 215	
cga aac aaa ggg caa ctt gta gac cca cgt ggt tcc aat act agt tca	785
Arg Asn Lys Gly Gln Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser	
220 225 230 235	
gct gat atc caa cta aag ctt aag gag caa agt gac aca ctt tgg aag	833
Ala Asp Ile Gln Leu Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys	
240 245 250	
tta aag gat gga ctt aag act cat gta tcg gct gct gaa tta agg gat	881
Leu Lys Asp Gly Leu Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp	
255 260 265	
atg ctt gag gct aat ggg cag gat aca tca gga cca gaa agg cac cta	929
Met Leu Glu Ala Asn Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu	
270 275 280	
ttg gat cgc tgt gcg gat gga atg ata ttt gga gcg ctg ggt cct tgc	977
Leu Asp Arg Cys Ala Asp Gly Met Ile Phe Gly Ala Leu Gly Pro Cys	
285 290 295	
cca gtc tgt gct aat ggc atg tac tat tat aat ggt cag tac caa tgc	1025
Pro Val Cys Ala Asn Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys	
300 305 310 315	
agt ggt aat gtg tca gag tgg tcc aag tgt aca tac tct gcc aca gaa	1073
Ser Gly Asn Val Ser Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu	
320 325 330	
cct gtc cgc gtt aag aag aag tgg caa att cca cat gga aca aag aat	1121
Pro Val Arg Val Lys Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn	
335 340 345	
gat tac ctt atg aag tgg ttc aaa tct caa aag gtt aag aaa cca gag	1169
Asp Tyr Leu Met Lys Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu	
350 355 360	
agg gtt ctt cca cca atg tca cct gag aaa tct gga agt aaa gca act	1217
Arg Val Leu Pro Pro Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr	
365 370 375	
cag aga aca tca ttg ctg tct tct aaa ggg ttg gat aaa tta agg ttt	1265
Gln Arg Thr Ser Leu Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe	
380 385 390 395	
tct gtt gta gga caa tca aaa gaa gca gca aat gag tgg att gag aag	1313
Ser Val Val Gly Gln Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys	
400 405 410	
ctc aaa ctt gct ggt gcc aac ttc tat gcc agg gtt gtc aaa gat att	1361
Leu Lys Leu Ala Gly Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile	
415 420 425	
gat tgt tta att gca tgt ggt gag ctc gac aat gaa aat gct gaa gtc	1409

Asp Cys Leu Ile Ala Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val	
430 435 440	
agg aaa gca agg agg ctg aag ata cca att gta agg gag ggt tac att	1457
Arg Lys Ala Arg Arg Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile	
445 450 455	
gga gaa tgt gtt aaa aag aac aaa atg ctg cca ttt gat ttg tat aaa	1505
Gly Glu Cys Val Lys Lys Asn Lys Met Leu Pro Phe Asp Leu Tyr Lys	
460 465 470 475	
cta gag aat gcc tta gag tcc tca aaa ggc agt act gtc act gtt aaa	1553
Leu Glu Asn Ala Leu Glu Ser Ser Lys Gly Ser Thr Val Thr Val Lys	
480 485 490	
gtt aag ggc cga agt gct gtt cat gag tcc tct ggt ttg caa gat act	1601
Val Lys Gly Arg Ser Ala Val His Glu Ser Ser Gly Leu Gln Asp Thr	
495 500 505	
gct cac att ctt gaa gat ggg aaa agc ata tac aat gca acc tta aac	1649
Ala His Ile Leu Glu Asp Gly Lys Ser Ile Tyr Asn Ala Thr Leu Asn	
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Met Ser Asp Leu Ala Leu Gly Val Asn Ser Tyr Tyr Val Leu Gln Ile	
525 530 535	
att gaa cag gat gat ggg tct gag tgc tac gta ttt cgt aag tgg gga	1745
Ile Glu Gln Asp Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly	
540 545 550 555	
cgg gtt ggg agt gag aaa att gga ggg caa aaa ctg gag gag atg tca	1793
Arg Val Gly Ser Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser	
560 565 570	
aaa act gag gca atc aag gaa ttc aaa aga tta ttt ctt gag aag act	1841
Lys Thr Glu Ala Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr	
575 580 585	
gga aac tca tgg gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag	1889
Gly Asn Ser Trp Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln	
590 595 600	
cct ggg aga ttt tac cca ctt gat gtt gat tat ggt gtt aag aaa gca	1937
Pro Gly Arg Phe Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala	
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cca aaa cgg aaa gat atc agt gaa atg aaa agt tct ctt gct cct caa	1985
Pro Lys Arg Lys Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln	
620 625 630 635	
ttg cta gaa ctc atg aag atg ctt ttc aat gtg gag aca tat aga gct	2033
Leu Leu Glu Leu Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala	
640 645 650	
gct atg atg gaa ttt gaa att aat atg tca gaa atg cct ctt ggg aag	2081
Ala Met Met Glu Phe Glu Ile Asn Met Ser Glu Met Pro Leu Gly Lys	
655 660 665	
cta agc aag gaa aat att gag aaa gga ttt gaa gca tta act gag ata	2129
Leu Ser Lys Glu Asn Ile Glu Lys Gly Phe Glu Ala Leu Thr Glu Ile	
670 675 680	
cag aat tta ttg aag gac acc gct gat caa gca ctg gct gtt aga gaa	2177
Gln Asn Leu Leu Lys Asp Thr Ala Asp Gln Ala Leu Ala Val Arg Glu	
685 690 695	

agc tta att gtt gct gcg agc aat cgc ttt ttc act ctt atc cct tct	2225
Ser Leu Ile Val Ala Ala Ser Asn Arg Phe Phe Thr Leu Ile Pro Ser	
700 705 710 715	
att cat cct cat att ata cgg gat gag gat gat ttg atg atc aaa gcg	2273
Ile His Pro His Ile Ile Arg Asp Glu Asp Asp Leu Met Ile Lys Ala	
720 725 730	
aaa atg ctt gaa gct ctg cag gat att gaa att gct tca aag ata gtt	2321
Lys Met Leu Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val	
735 740 745	
ggc ttc gat agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa	2369
Gly Phe Asp Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys	
750 755 760	
ctt cac tgt gac atc acc ccg ctg gct cac gat agt gaa gat tac aag	2417
Leu His Cys Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys	
765 770 775	
tta att gag cag tat ctc ctc aac aca cat gct cct act cac aag gac	2465
Leu Ile Glu Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp	
780 785 790 795	
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Trp Ser Leu Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu	
800 805 810	
ctt aat aag tac tca aga tat aaa aat aat ctg cat aac aag atg cta	2561
Leu Asn Lys Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu	
815 820 825	
tta tgg cac ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa	2609
Leu Trp His Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln	
830 835 840	
ggg cta aga att gca cct cct gag gca cct gtt act ggc tat atg ttc	2657
Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe	
845 850 855	
ggc aaa ggc ctc tac ttt gca gat cta gta agc aag agc gca caa tac	2705
Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr	
860 865 870 875	
tgt tat gtg gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag	2753
Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu	
880 885 890	
gtt gct tta gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac	2801
Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp	
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aaa cct cca aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg	2849
Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val	
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cca ctg gag tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc	2897
Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro	
925 930 935	
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Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr	
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aat gag tac atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg	2993
Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu	
960 965 970	

ctg aag gtg cgt ttc cat cac aag agg tagctgggag actaggcaag 3040
 Leu Lys Val Arg Phe His His Lys Arg
 975 980

tagagttgga aggtagagaa gcagagttag gcgatgcctc ttttgggtatt attagtaagc 3100
 ctggcatgta tttatgggtg ctgcgccttg atccattttg gtaagtgttg cttgggcatc 3160
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 35 40 45
 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
 50 55 60
 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
 65 70 75 80
 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
 85 90 95
 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
 100 105 110
 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
 115 120 125
 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
 130 135 140
 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
 145 150 155 160
 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
 165 170 175
 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
 180 185 190
 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
 195 200 205
 Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
 210 215 220
 Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
 225 230 235 240
 Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
 245 250 255
 Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn

260

265

270

Gly	Gln	Asp	Thr	Ser	Gly	Pro	Glu	Arg	His	Leu	Leu	Asp	Arg	Cys	Ala		
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Asp	Gly	Met	Ile	Phe	Gly	Ala	Leu	Gly	Pro	Cys	Pro	Val	Cys	Ala	Asn		
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Gly	Met	Tyr	Tyr	Tyr	Asn	Gly	Gln	Tyr	Gln	Cys	Ser	Gly	Asn	Val	Ser		
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Glu	Trp	Ser	Lys	Cys	Thr	Tyr	Ser	Ala	Thr	Glu	Pro	Val	Arg	Val	Lys		
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Lys	Lys	Trp	Gln	Ile	Pro	His	Gly	Thr	Lys	Asn	Asp	Tyr	Leu	Met	Lys		
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Trp	Phe	Lys	Ser	Gln	Lys	Val	Lys	Lys	Pro	Glu	Arg	Val	Leu	Pro	Pro		
	355						360					365					
Met	Ser	Pro	Glu	Lys	Ser	Gly	Ser	Lys	Ala	Thr	Gln	Arg	Thr	Ser	Leu		
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Leu	Ser	Ser	Lys	Gly	Leu	Asp	Lys	Leu	Arg	Phe	Ser	Val	Val	Gly	Gln		
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Ser	Lys	Glu	Ala	Ala	Asn	Glu	Trp	Ile	Glu	Lys	Leu	Lys	Leu	Ala	Gly		
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Ala	Asn	Phe	Tyr	Ala	Arg	Val	Val	Lys	Asp	Ile	Asp	Cys	Leu	Ile	Ala		
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Cys	Gly	Glu	Leu	Asp	Asn	Glu	Asn	Ala	Glu	Val	Arg	Lys	Ala	Arg	Arg		
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Leu	Lys	Ile	Pro	Ile	Val	Arg	Glu	Gly	Tyr	Ile	Gly	Glu	Cys	Val	Lys		
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Lys	Asn	Lys	Met	Leu	Pro	Phe	Asp	Leu	Tyr	Lys	Leu	Glu	Asn	Ala	Leu		
465					470					475					480		
Glu	Ser	Ser	Lys	Gly	Ser	Thr	Val	Thr	Val	Lys	Val	Lys	Gly	Arg	Ser		
				485					490					495			
Ala	Val	His	Glu	Ser	Ser	Gly	Leu	Gln	Asp	Thr	Ala	His	Ile	Leu	Glu		
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Asp	Gly	Lys	Ser	Ile	Tyr	Asn	Ala	Thr	Leu	Asn	Met	Ser	Asp	Leu	Ala		
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Leu	Gly	Val	Asn	Ser	Tyr	Tyr	Val	Leu	Gln	Ile	Ile	Glu	Gln	Asp	Asp		
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Gly	Ser	Glu	Cys	Tyr	Val	Phe	Arg	Lys	Trp	Gly	Arg	Val	Gly	Ser	Glu		
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Lys	Ile	Gly	Gly	Gln	Lys	Leu	Glu	Glu	Met	Ser	Lys	Thr	Glu	Ala	Ile		
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Lys	Glu	Phe	Lys	Arg	Leu	Phe	Leu	Glu	Lys	Thr	Gly	Asn	Ser	Trp	Glu		
			580					585					590				
Ala	Trp	Glu	Cys	Lys	Thr	Asn	Phe	Arg	Lys	Gln	Pro	Gly	Arg	Phe	Tyr		
	595						600					605					
Pro	Leu	Asp	Val	Asp	Tyr	Gly	Val	Lys	Lys	Ala	Pro	Lys	Arg	Lys	Asp		
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Ile	Ser	Glu	Met	Lys	Ser	Ser	Leu	Ala	Pro	Gln	Leu	Leu	Glu	Leu	Met	
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Lys	Met	Leu	Phe	Asn	Val	Glu	Thr	Tyr	Arg	Ala	Ala	Met	Met	Glu	Phe	
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	690					695					700					
Ala	Ser	Asn	Arg	Phe	Phe	Thr	Leu	Ile	Pro	Ser	Ile	His	Pro	His	Ile	
705					710					715					720	
Ile	Arg	Asp	Glu	Asp	Asp	Leu	Met	Ile	Lys	Ala	Lys	Met	Leu	Glu	Ala	
				725					730					735		
Leu	Gln	Asp	Ile	Glu	Ile	Ala	Ser	Lys	Ile	Val	Gly	Phe	Asp	Ser	Asp	
			740					745					750			
Ser	Asp	Glu	Ser	Leu	Asp	Asp	Lys	Tyr	Met	Lys	Leu	His	Cys	Asp	Ile	
		755					760					765				
Thr	Pro	Leu	Ala	His	Asp	Ser	Glu	Asp	Tyr	Lys	Leu	Ile	Glu	Gln	Tyr	
	770					775					780					
Leu	Leu	Asn	Thr	His	Ala	Pro	Thr	His	Lys	Asp	Trp	Ser	Leu	Glu	Leu	
785					790					795					800	
Glu	Glu	Val	Phe	Ser	Leu	Asp	Arg	Asp	Gly	Glu	Leu	Asn	Lys	Tyr	Ser	
				805					810					815		
Arg	Tyr	Lys	Asn	Asn	Leu	His	Asn	Lys	Met	Leu	Leu	Trp	His	Gly	Ser	
			820					825					830			
Arg	Leu	Thr	Asn	Phe	Val	Gly	Ile	Leu	Ser	Gln	Gly	Leu	Arg	Ile	Ala	
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Pro	Pro	Glu	Ala	Pro	Val	Thr	Gly	Tyr	Met	Phe	Gly	Lys	Gly	Leu	Tyr	
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Phe	Ala	Asp	Leu	Val	Ser	Lys	Ser	Ala	Gln	Tyr	Cys	Tyr	Val	Asp	Arg	
865					870					875					880	
Asn	Asn	Pro	Val	Gly	Leu	Met	Leu	Leu	Ser	Glu	Val	Ala	Leu	Gly	Asp	
				885					890					895		
Met	Tyr	Glu	Leu	Lys	Lys	Ala	Thr	Ser	Met	Asp	Lys	Pro	Pro	Arg	Gly	
			900					905					910			
Lys	His	Ser	Thr	Lys	Gly	Leu	Gly	Lys	Thr	Val	Pro	Leu	Glu	Ser	Glu	
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Phe	Val	Lys	Trp	Arg	Asp	Asp	Val	Val	Val	Pro	Cys	Gly	Lys	Pro	Val	
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Pro	Ser	Ser	Ile	Arg	Ser	Ser	Glu	Leu	Met	Tyr	Asn	Glu	Tyr	Ile	Val	
945					950					955					960	
Tyr	Asn	Thr	Ser	Gln	Val	Lys	Met	Gln	Phe	Leu	Leu	Lys	Val	Arg	Phe	
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His His Lys Arg
980

<210> 12
<211> 1010
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: fusion protein
between APP N-terminal domain and GUS protein

<400> 12

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Glu	Glu	Ala	Ile	Ala	Glu	Asp	Thr	Lys	Lys	Glu	Glu	Ser	Lys	Ser	Lys	35	40	45	
Arg	Lys	Arg	Asn	Ser	Ser	Asn	Asp	Thr	Tyr	Glu	Ser	Asn	Lys	Leu	Ile	50	55	60	
Ala	Ile	Gly	Glu	Phe	Arg	Gly	Met	Ile	Val	Lys	Glu	Leu	Arg	Glu	Glu	65	70	75	80
Ala	Ile	Lys	Arg	Gly	Leu	Asp	Thr	Thr	Gly	Thr	Lys	Lys	Asp	Leu	Leu	85	90	95	
Glu	Arg	Leu	Cys	Asn	Asp	Ala	Asn	Asn	Val	Ser	Asn	Ala	Pro	Val	Lys	100	105	110	
Ser	Ser	Asn	Gly	Thr	Asp	Glu	Ala	Glu	Asp	Asp	Asn	Asn	Gly	Phe	Glu	115	120	125	
Glu	Glu	Lys	Lys	Glu	Glu	Lys	Ile	Val	Thr	Ala	Thr	Lys	Lys	Gly	Ala	130	135	140	
Ala	Val	Leu	Asp	Gln	Trp	Ile	Pro	Asp	Glu	Ile	Lys	Ser	Gln	Tyr	His	145	150	155	160
Val	Leu	Gln	Arg	Gly	Asp	Asp	Val	Tyr	Asp	Ala	Ile	Leu	Asn	Gln	Thr	165	170	175	
Asn	Val	Arg	Asp	Asn	Asn	Asn	Lys	Phe	Phe	Val	Leu	Gln	Val	Leu	Glu	180	185	190	
Ser	Asp	Ser	Lys	Lys	Thr	Tyr	Met	Val	Tyr	Thr	Arg	Trp	Gly	Arg	Val	195	200	205	
Gly	Val	Lys	Gly	Gln	Ser	Lys	Leu	Asp	Gly	Pro	Tyr	Asp	Ser	Trp	Asp	210	215	220	
Arg	Ala	Ile	Glu	Ile	Phe	Thr	Asn	Lys	Phe	Asn	Asp	Lys	Thr	Lys	Asn	225	230	235	240
Tyr	Trp	Ser	Asp	Arg	Lys	Glu	Phe	Ile	Pro	His	Pro	Lys	Ser	Tyr	Thr	245	250	255	
Trp	Leu	Glu	Met	Asp	Tyr	Gly	Lys	Glu	Glu	Asn	Asp	Ser	Pro	Val	Asn	260	265	270	
Asn	Asp	Ile	Pro	Ser	Ser	Ser	Ser	Glu	Val	Lys	Pro	Glu	Gln	Ser	Lys	275	280	285	

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Met	Met	Ala	Gln	His	Met	Met	Glu	Ile	Gly	Tyr	Asn	Ala	Asn	Lys	Leu		
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Pro	Leu	Gly	Lys	Ile	Ser	Lys	Ser	Thr	Ile	Ser	Lys	Gly	Tyr	Glu	Val		
				325					330					335			
Leu	Lys	Arg	Ile	Ser	Glu	Val	Ile	Asp	Arg	Tyr	Asp	Arg	Thr	Arg	Leu		
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Glu	Glu	Leu	Ser	Gly	Glu	Phe	Tyr	Thr	Val	Ile	Pro	His	Asp	Phe	Gly		
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Phe	Lys	Lys	Met	Ser	Gln	Phe	Val	Ile	Asp	Thr	Pro	Gln	Lys	Leu	Lys		
370						375					380						
Gln	Lys	Ile	Glu	Met	Val	Glu	Ala	Leu	Gly	Glu	Ile	Glu	Leu	Ala	Thr		
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Lys	Leu	Leu	Ser	Val	Asp	Pro	Met	Val	Arg	Pro	Val	Glu	Thr	Pro	Thr		
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Glu	Asn	Cys	Gly	Ile	Asp	Gln	Arg	Trp	Trp	Glu	Ser	Ala	Leu	Gln	Glu		
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Ser	Arg	Ala	Ile	Ala	Val	Pro	Gly	Ser	Phe	Asn	Asp	Gln	Phe	Ala	Asp		
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Ala	Asp	Ile	Arg	Asn	Tyr	Ala	Gly	Asn	Val	Trp	Tyr	Gln	Arg	Glu	Val		
465					470					475					480		
Phe	Ile	Pro	Lys	Gly	Trp	Ala	Gly	Gln	Arg	Ile	Val	Leu	Arg	Phe	Asp		
			485					490						495			
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			580					585					590				
Asp	Ile	Thr	Val	Val	Thr	His	Val	Ala	Gln	Asp	Cys	Asn	His	Ala	Ser		
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Leu Gln Val Val Asn Pro His Leu Trp Gln Pro Gly Glu Gly Tyr Leu
 645 650 655
 Tyr Glu Leu Cys Val Thr Ala Lys Ser Gln Thr Glu Cys Asp Ile Tyr
 660 665 670
 Pro Leu Arg Val Gly Ile Arg Ser Val Ala Val Lys Gly Glu Gln Phe
 675 680 685
 Leu Ile Asn His Lys Pro Phe Tyr Phe Thr Gly Phe Gly Arg His Glu
 690 695 700
 Asp Ala Asp Leu Arg Gly Lys Gly Phe Asp Asn Val Leu Met Val His
 705 710 715 720
 Asp His Ala Leu Met Asp Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser
 725 730 735
 His Tyr Pro Tyr Ala Glu Glu Met Leu Asp Trp Ala Asp Glu His Gly
 740 745 750
 Ile Val Val Ile Asp Glu Thr Ala Ala Val Gly Phe Asn Leu Ser Leu
 755 760 765
 Gly Ile Gly Phe Glu Ala Gly Asn Lys Pro Lys Glu Leu Tyr Ser Glu
 770 775 780
 Glu Ala Val Asn Gly Glu Thr Gln Gln Ala His Leu Gln Ala Ile Lys
 785 790 795 800
 Glu Leu Ile Ala Arg Asp Lys Asn His Pro Ser Val Val Met Trp Ser
 805 810 815
 Ile Ala Asn Glu Pro Asp Thr Arg Pro Gln Gly Ala Arg Glu Tyr Phe
 820 825 830
 Ala Pro Leu Ala Glu Ala Thr Arg Lys Leu Asp Pro Thr Arg Pro Ile
 835 840 845
 Thr Cys Val Asn Val Met Phe Cys Asp Ala His Thr Asp Thr Ile Ser
 850 855 860
 Asp Leu Phe Asp Val Leu Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val
 865 870 875 880
 Gln Ser Gly Asp Leu Glu Thr Ala Glu Lys Val Leu Glu Lys Glu Leu
 885 890 895
 Leu Ala Trp Gln Glu Lys Leu His Gln Pro Ile Ile Ile Thr Glu Tyr
 900 905 910
 Gly Val Asp Thr Leu Ala Gly Leu His Ser Met Tyr Thr Asp Met Trp
 915 920 925
 Ser Glu Glu Tyr Gln Cys Ala Trp Leu Asp Met Tyr His Arg Val Phe
 930 935 940
 Asp Arg Val Ser Ala Val Val Gly Glu Gln Val Trp Asn Phe Ala Asp
 945 950 955 960
 Phe Ala Thr Ser Gln Gly Ile Leu Arg Val Gly Gly Asn Lys Lys Gly
 965 970 975
 Ile Phe Thr Arg Asp Arg Lys Pro Lys Ser Ala Ala Phe Leu Leu Gln
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 Lys Arg Trp Thr Gly Met Asn Phe Gly Glu Lys Pro Gln Gln Gly Gly

995

1000

1005

Lys Gln
1010

<210> 13

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerated
PCR primer

<400> 13

ccgaattcgg ntayatgtty ggnaa

25

<210> 14

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerated
PCR primer

<400> 14

ccgaattcac natrtaytcr ttrta

25

<210> 15

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide
for use as PCR primer

<400> 15

gggaccatgt agtttatctt gacct

25

<210> 16

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide for use in PCR

<400> 16

gacctcgtac cccaactctt ccccat

26

<210> 17

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide for use in PCR

<400> 17
aagtcgacgc ggccgccaca cctagtgccca ggtcag 36

<210> 18
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide for use in PCR

<400> 18
atctcaattg tacatttctc agga 24

<210> 19
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide for use in PCR

<400> 19
aggatcccat ggcgaacaag ctcaaagtga c 31

<210> 20
<211> 26
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide for use in PCR

<400> 20
aggatcctta gtgctttag tagtgaat 26

<210> 21
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<223> Description of Artificial Sequence: APP promoter
fusion with beta-glucuronidase gene

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<222> (1)..(1961)

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<222> (1962)..(1964)
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